

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/935, 144 A  
Source: FW16  
Date Processed by STIC: 1-13-05

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IFW16

## RAW SEQUENCE LISTING

DATE: 01/13/2005

PATENT APPLICATION: US/09/935,144A

TIME: 17:43:12

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3 <110> APPLICANT: LARSEN, GLENN R.  
 4 SAKO, DIANNE S.  
 5 CHANG, XIAO-JIA  
 6 VELDMAN, GEERTRUIDA M.  
 7 CUMMING, DALE  
 8 KUMAR, RAVINDRA  
 9 SHAW, GRAY  
 11 <120> TITLE OF INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN  
 13 <130> FILE REFERENCE: 08702.0010-12000  
 15 <140> CURRENT APPLICATION NUMBER: 09/935,144A  
 16 <141> CURRENT FILING DATE: 2001-08-21  
 18 <150> PRIOR APPLICATION NUMBER: 08/713,556  
 19 <151> PRIOR FILING DATE: 1996-08-30  
 21 <150> PRIOR APPLICATION NUMBER: 08/428,734  
 22 <151> PRIOR FILING DATE: 1995-04-25  
 24 <150> PRIOR APPLICATION NUMBER: 08/316,305  
 25 <151> PRIOR FILING DATE: 1994-09-30  
 27 <150> PRIOR APPLICATION NUMBER: 08/235,398  
 28 <151> PRIOR FILING DATE: 1994-04-28  
 30 <150> PRIOR APPLICATION NUMBER: 08/112,608  
 31 <151> PRIOR FILING DATE: 1993-08-26  
 33 <150> PRIOR APPLICATION NUMBER: 07/965,662  
 34 <151> PRIOR FILING DATE: 1992-10-23  
 36 <150> PRIOR APPLICATION NUMBER: PCT/US93/10168  
 37 <151> PRIOR FILING DATE: 1993-10-22  
 39 <160> NUMBER OF SEQ ID NOS: 48  
 41 <170> SOFTWARE: PatentIn Ver. 3.2  
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 56 Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn  
 57 1 5 10 15  
 59 agc ttg cag ctg tgg gac acc tgg gca gat gaa gcc gag aaa gcc ttg 155  
 60 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu  
 61 20 25 30  
 63 ggt ccc ctg ctt gcc cgg gac cgg aga cag gcc acc gaa tat gag tac 203

(pg. 6)

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68	Leu	Asp	Tyr	Asp	Phe	Leu	Pro	Glu	Thr	Glu	Pro	Pro	Glu	Met	Leu	Arg		
69			50				55					60						
71	aac	agc	act	gac	acc	act	cct	ctg	act	ggg	cct	gga	acc	cct	gag	tct	299	
72	Asn	Ser	Thr	Asp	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gly	Thr	Pro	Glu	Ser		
73	65					70				75					80			
75	acc	act	gtg	gag	cct	gct	gca	agg	cgt	tct	act	ggc	ctg	gat	gca	gga	347	
76	Thr	Thr	Val	Glu	Pro	Ala	Ala	Arg	Arg	Ser	Thr	Gly	Leu	Asp	Ala	Gly		
77					85					90					95			
79	ggg	gca	gtc	aca	gag	ctg	acc	acg	gag	ctg	gcc	aac	atg	ggg	aac	ctg	395	
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81			100						105					110				
83	tcc	acg	gat	tca	gca	gct	atg	gag	ata	cag	acc	act	caa	cca	gca	gcc	443	
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92	Arg	Leu	Thr	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Pro	Leu	Ala	Ala	Thr	Glu		
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96	Ala	Gln	Thr	Thr	Pro	Pro	Ala	Ala	Thr	Glu	Ala	Gln	Thr	Thr	Gln	Pro		
97				165					170					175				
99	aca	ggc	ctg	gag	gca	cag	acc	act	gca	cca	gca	gcc	atg	gag	gca	cag	635	
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121				260					265					270				
123	ttc	ata	ccc	ttt	tct	gtg	tcc	tct	gtt	act	cac	aag	ggc	att	ccc	atg	923	
124	Phe	Ile	Pro	Phe	Ser	Val	Ser	Ser	Val	Thr	His	Lys	Gly	Ile	Pro	Met		
125			275					280					285					
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128	Ala	Ala	Ser	Asn	Leu	Ser	Val	Asn	Tyr	Pro	Val	Gly	Ala	Pro	Asp	His		

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132 Ile Ser Val Lys Gln Cys Leu Leu Ala Ile Leu Ile Leu Ala Leu Val
133 305      310      315      320
135 gcc act atc ttc ttc gtg tgc act gtg gtg ctg gcg gtc cgc ctc tcc 1067
136 Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
137      325      330      335
139 cgc aag ggc cac atg tac ccc gtg cgt aat tac tcc ccc acc gag atg 1115
140 Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
141      340      345      350
143 gtc tgc atc tca tcc ctg ttg cct gat ggg ggt gag ggg ccc tct gcc 1163
144 Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
145      355      360      365
147 aca gcc aat ggg ggc ctg tcc aag gcc aag agc ccg ggc ctg acg cca 1211
148 Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
149      370      375      380
151 gag ccc agg gag gac cgt gag ggg gat gac ctc acc ctg cac agc ttc 1259
152 Glu Pro Arg Glu Asp Arg Glu Gly Asp Asp Leu Thr Leu His Ser Phe
153 385      390      395      400
155 ctc cct tag ctactctgc catctgtttt ggcaagaccc cacctccacg 1308
156 Leu Pro
158 ggctctcctg ggccaccctc gagtgccag accccaatcc acagctctgg gcttcctcgg 1368
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185 35 40 45
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191 65 70 75 80
193 Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
194 85 90 95
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211 Thr Gly Leu Glu Ala Gln Thr Thr Ala Pro Ala Ala Met Glu Ala Gln
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221 225      230      235      240
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232 Ala Ala Ser Asn Leu Ser Val Asn Tyr Pro Val Gly Ala Pro Asp His
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235 Ile Ser Val Lys Gln Cys Leu Leu Ala Ile Leu Ile Leu Ala Leu Val
236 305      310      315      320
238 Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
239      325      330      335
241 Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
242      340      345      350
244 Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
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247 Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
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269 1 5 10 15
271 agc ttg cag ctg tgg gac acc tgg gca gat gaa gcc gag aaa gcc ttg 96
272 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
273 20 25 30
275 ggt ccc ctg ctt gcc cgg gac cgg aga cag gcc acc gaa tat gag tac 144

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:47; Xaa Pos. 2,8,9,10

**VERIFICATION SUMMARY**

DATE: 01/13/2005

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Input Set : **A:\87021012.app**Output Set: **N:\CRF4\01132005\I935144A.raw**

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